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QY 117 SSKATPPSVYPLAPGCGDTGSSVTLGCLVKGPEPESTVTWNSGSLSSSVHTFPALQ 176
|:|||||:|||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 112 SNAKTPPSPVPLAPGSAQNTSMVTLGCLVKGPEPESTVTWNSGSLSSSVHTFPALQ 171
QY 177 SGLYTWSSSVYVPSSTWSPSQVTCVAHPASSTYVDKLEPSGPISITINCPCKECHKC 236
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 172 SLYLTSSSVYVPSSTWSPSETVTCVAHPASSTYVDKLEPSGPISITINCPCKECHKC 222
QY 237 PAPNLEGGSVFPEPPNIDVIMSLTPKVTGVYVDSDDDPVOISWPNVNEVTAQT 296
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 223 TYPEVS---SVLEPPKPKVDVLTITLTPKVTGVYVDSKDDPEVQPSWFDVDEVTAAQT 279
QY 297 QTHREDYNSTIRVSTLPIQHDMSGKEFEKCKVNNKDLPSPIERTISKIKGLVAPQVY 356
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 280 QPREQFNSTFPVSSELPIMHODMLNGKEFKCRVNSAARPAIEKTIKTKGKPAQVY 339
QY 357 ILPPAEBOLSKRDVSLTCLVAGFNPQDISVEVTSNGHTEENKDTAPVLDSDGTYFYSK 416
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 340 ILPPKPEQMAKDKVSLTCLMITEFFPEDITVEWQMGAPAEYKNKTIQPIMDTGSYFVYSK 399
QY 417 LMKTKSKWEKTDSESCNVRHEGLKNYLTCKTISRSPK 454
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 400 LNVQKSNMEAGNFTCTSVLHEGLNHNTEKMLNLSHSPK 437

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RESULT 2
Q9NPP6 PRELIMINARY: PRT: 416 AA.
AC Q9NPP6:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN VARIANT (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RA Auffray C., Ansoorge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.;
RL "The European Image consortium for integrated Molecular analysis of
human gene transcripts";
RT Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
KL EMBL; AL389978; CAB97534.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE 416 AA; 44786 MW; 8C41708BB8A4687 CRC64;

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Query Match 22.4%; Score 543; DB 4; Length 416;  
 Best Local Similarity 33.3%; Pred. No. 6.3e-35;  
 Matches 143; Conservative 76; Mismatches 162; Indels 48; Gaps 19;

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QY 42 GSELMIGINYYGSGIFSPKFKATLTVDKSSSTAVMELSLTSESAVYYCARRAG 101
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 2 GKGLKVVSVISSGDTVDVDSVKGFTVSRPTAKNSLSLQSSSLVEETAVYYCAR--- 58
QY 102 AYY-EDYWGQGTTLTVSSAKTTPPSVYPLAPGCGDT--GSSVTLGCLVKGPE-ESVTV 157
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 59 TYGDMVGQGTTVYSSASPTSPKVFPLST---DSTPDGDNVYVACLVGFGFPQEPISLV 115
QY 158 TWNSGSLSSSVHTFPALQSG--LVTWSSSVYVPSSTWSP-SQVTCVAH---PASSTTV 211
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

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Db 116 TWSESGQNTANRFPSPQDASGLYTTSSQLTLPATQCPDGKSVTCNVKHYTNPSQVTV 175
QY 212 DKLEPSGFIITINPCPPCKECHKCAPULEGGSVFIRPPINKIVIMSLTPKTCVAV 271
Db 176 P-----CVPPEPPC-CH-----PRSLRPALEDLLGAS-EANLTCTLT 213
QY 272 DYSEDDPDVQISMFVNNVHTAQTQTHREDYNSTIRVSTLPIQHDMSGKEFEKCKVN 331
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 214 GL-RDASGATFTWTPSSSK--SAVQGPPEPRLCGCVSVSSVLPGAQAPWNHGEFTCTAA 270
QY 332 NKDLSPERTISKIKGLVAPQVYILPPAEBOLSKRD-VSLTCLVAGFNPQDISVEVTS 390
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 271 HPELKTPLTANITK-SGNTFREPHLLPPSEBLINELVTLTCLARGSPKVDVLRMLQ 329
QY 391 NGH--TEENYKDTAPVLD-SDG--SYFIYSKLMNMTSKWEKTDSESCNVRHEGLKNYLT 445
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 330 GSOELPREKYLWASRQESQGTTFPAVSIILRVAEDMKDKDTSCNVGHEALPLATFQ 389
QY 446 KTISRSPK 454
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 390 KTIDRLAGK 398

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RESULT 3
Q9QXF0 PRELIMINARY: PRT: 117 AA.
AC Q9QXF0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

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Query Match 19.8%; Score 480.5; DB 11; Length 117;  
 Best Local Similarity 78.8%; Pred. No. 1.1e-30;  
 Matches 93; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

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QY 1 EVOLDOOSGPELVKPAASWISCRISATYFTENTVIMVKOSHGESLEMTGGINPYIGSIF 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 EVOLDOOSGPELVKPAASWISCRISATYFTENTVIMVKOSHGESLEMTGGINPYIGSIF 60
QY 61 SPKFKGATLTVDKSSSTAVMELSLTSEDSAVYYCARRAGAYYDYWGQGTTLTVSS 118
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 NQKFKGATLTVDKSSSTAVMELSLTSEDSAVYYCARRAGAYYDYWGQGTTLTVSS 117

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RESULT 4
Q9UP60 PRELIMINARY: PRT: 384 AA.
AC Q9UP60:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE SNCT3 PROTEIN.
GN SNCT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C;  
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,  
RA Mattis L.M., Evans M.J.;  
RT "Humanized porcine VCAH-specific monoclonal antibodies with chimeric  
RT IgG2/G4 constant regions block human leukocyte binding to porcine  
RT endothelial cells."  
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
CC DOMAIN  
DR EMBL: U78801; AAD00293.1; -  
DR InterPro: IPR003006; -  
DR InterPro: IPR003596; -  
DR Pfam: PF00047; 1g; 1.  
DR SMART: SM00406; 1g; 1.  
FT NON\_TER 1  
FT SEQUENCE 118 AA; 13036 MW; 90EBC559D31EC4FC CRC64;

Query Match  
Best Local Similarity 16.5%; Score 401; DB 11; Length 118;  
Matches 77; Conservative 12; Mismatches 29; Indels 0; Gaps 0;

OY 1 EVOLQSGPELVPGASVMISCTSAFTTENTVHWKSHGSELMIGINPYGSGIF 60  
DB 1 QVQVQSGAEIARPMASVKLSKASGYNFSYMWKQKRGGLMIGALYPGDDTSY 60  
OY 61 SPFKKATITVDKSSSTAYMELRLTSDSAVYCARAGAYFPYWGQTTLVSS 118  
DB 61 TQFKRKATITLADKSSSTAYMQLSLSDSAVYCARIVGCGYFDYWGQTTLVSS 118

RESULT 8  
ID 09JUL81 PRELIMINARY; PRT; 114 AA.

AC 09JUL81;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE ANTI-MIOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-  
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF206025; AAF69323.1; -  
DR InterPro: IPR003006; -  
DR InterPro: IPR003596; -  
DR Pfam: PF00047; 1g; 1.  
DR SMART: SM00406; 1g; 1.  
FT NON\_TER 1  
FT NON\_TER 114  
FT SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

Query Match  
Best Local Similarity 15.9%; Score 385; DB 11; Length 114;  
Matches 76; Conservative 11; Mismatches 23; Indels 4; Gaps 1;

OY 9 PELVVRGASVMISCTSAFTTENTVHWKSHGSELMIGINPYGSGIFSPKFKGA 68  
DB 1 POLVVRGASVVKISCKASGYSFTSYMWKQKRGGLMIGALYPGDDTSY 60  
OY 69 TLVVDKSSSTAYMELRLTSDSAVYCARAGAYFPYWGQTTLVSS 118  
DB 69 TLVVDKSSSTAYMELRLTSDSAVYCARAGAYFPYWGQTTLVSS 118

DB 61 TLVVDKSSSTAYMQLSLSDSAVYCARSNYGSLLYFDYWGQTTLVSS 114

RESULT 9  
ID 09JUL77 PRELIMINARY; PRT; 110 AA.

AC 09JUL77;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE ANTI-MIOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-DHA/2;  
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;  
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-  
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF206029; AAF69327.1; -  
DR InterPro: IPR003006; -  
DR InterPro: IPR003596; -  
DR Pfam: PF00047; 1g; 1.  
DR SMART: SM00406; 1g; 1.  
FT NON\_TER 1  
FT NON\_TER 110  
FT SEQUENCE 110 AA; 12138 MW; 2EDEB81FB5862C9AF CRC64;

Query Match  
Best Local Similarity 15.6%; Score 379; DB 11; Length 110;  
Matches 71; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

OY 11 LVKPGASVMISCTSAFTTENTVHWKSHGSELMIGINPYGSGIFSPKFKATL 70  
DB 3 LVKPGASVVKISCKASGYTTSWMHWKQKRGGLMIGALYPGDDTSY 62  
OY 71 TVDSSSTAYMELRLTSDSAVYCARAGAYFPYWGQTTLVSS 118  
DB 63 TVDSSSTAYMELRLTSDSAVYCARORRNRYAMDYWGQTSYTVSS 110

RESULT 10  
ID 090544 PRELIMINARY; PRT; 684 AA.

AC 090544;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE NOVEL ANTIGEN RECEPTOR PRECURSOR.  
OS Ginglymostoma citrullum (Nurse shark).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphi; Galeoidea; Orectolobiformes;  
OC Ginglymostomidae; Ginglymostoma.  
OX NCBI\_TaxID=7801;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SPLEEN;  
RX MEDLINE=95183140; PubMed=7877689;  
RA Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,  
RA Flajnik M.F.;  
RT "A new antigen receptor gene family that undergoes rearrangement and  
RT extensive somatic diversification in sharks."  
RL Nature 374:168-173(1995).  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
CC DOMAIN  
DR EMBL: U18701; AAB48195.1; -  
DR HSP: P01857; IFC1.  
DR InterPro: IPR003006; -  
DR InterPro: IPR003597; -

DR Pfam: PF00047; Ig; 6.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_3.  
 DR SMART: SM00407; IGc1; 1.  
 KM SIGNAL.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 684 NOVEL ANTIGEN RECEPTOR.  
 SQ SEQUENCE 684 AA; 75224 MW; 2FF9D2071CDA6D6D CRC64;

Query Match 15.3%; Score 372.5; DB 13; Length 684;  
 Best Local Similarity 23.6%; Pred. No. 3.3e-21;  
 Matches 130; Conservative 88; Mismatches 205; Indels 129; Gaps 23;

QY 2 VOLOQSGPELVKPGASVMISCRISATYFTEN-VYHW-----VQSHGE-43  
 DB 145 VSLHSAITEORANRFVOLVCLISGY-YPENIAVSQKQNKTKTSGFATSPVTKSSNDF-203  
 QY 44 ---SL-----EWIGGINPYGGSIFSPKFKATLTVD---KSSSTAYMELSLTSED-90  
 DB 204 SCASLAKVPLQEW-----SRGSVSCQVSHSATSSNQRKEISTEIAVLADPIYEE-256  
 QY 91 ----SAVYVC-----ARRAGAYF-----DY-107  
 DB 257 IWIDKSATLICEVLSTVSAGVYVSMVNGKYRNEGQMEPTKMGNOYLTLISRLTSYEE-316  
 QY 108 WGSTLTIVSS-----AKTTPSYVPIAAGCGD-ITGSSVTLCGLVKG-149  
 DB 317 WQSGVEYTCCKAKODOSTPVYKTRKARVEPTKPLRLPLPSPELIQSTSSATLTCLIRG-376  
 QY 150 YFPESVITVWNSSG--SLSSSVHPPALQSGL-YTMSSSVVPSPSTWPS-QVTVCVAHP-205  
 DB 377 FYPPKVSVMQKDVSVSANTNFPTALEDLTFSTRSLMLTAVENKSGAKYCTASHP-436  
 QY 206 ASSTVDPKLEPSPGPISTINCPCKECHKCPAPNLEGSPVFTEPPNIKDVLMISLTPK-265  
 DB 437 PSOSTVKRVIR-----NOKVDCROT-----DISVSLKPPFEET-WTOQTAT-477  
 QY 266 VTCVYVVDSEDDPDYQISWPFNNNEVHTAQOTHRREDYNSTIRVSTLPPIQHOMWSKE-325  
 DB 478 IVCEI--VYSLENIKVFQWONGVERKKGVETQNPWMSGSTVSKIKVWASMDSGTE-535  
 QY 326 FKCVNNKNDLPSPIERTISKIK-GLVRAPQVYLPPPAEOL-SRKDVSILTGLVGFNPGD-383  
 DB 536 YVCLVEDSELTPTPKASIRKRVNSQMPKRYLLHPSTEDIDENSATLKLAINFHPAE-595  
 QY 384 ISVEWISNGH-TEENYQDTAPVLDSDGSYFLYSKLNKTSKWEKTDSEFCNVREGLKNY-442  
 DB 596 IYVGWMANDTLIDSGRYQVDSEKSGSSPFVTDRLRLTAEMWNSDITYSCLVGHPSLNRD-655  
 QY 443 YLKTISRSPCK-454  
 DB 656 LIRST-NKSNCK-666

RESULT 11  
 Q9Y298 PRELIMINARY; PRT; 150 AA.  
 AC Q9Y298;  
 DT 01-NOV-1999 (Tremblrel, 12, Created)  
 DT 01-NOV-1999 (Tremblrel, 12, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel, 16, Last annotation update)  
 DE ICG VH PROTEIN PRECURSOR (FRAGMENT).  
 GN ICG VH.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98322155; Pubmed=9657749;  
 RA Jacquemin M.G., Vander Elst L.P.L.;  
 RT Mechanism and kinetics of factor VIII inactivation: study with an  
 RT IgG4 monoclonal antibody derived from a hemophilia A patient with

RT Inhibitor."  
 RL BLOD 92:496-506(1998).  
 CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AJ224083; CAA11829.1; -.  
 DR InterPro: IPR003006; -.  
 DR InterPro: IPR003596; -.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW SIGNAL.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT NON\_TER 150 150  
 SQ SEQUENCE 150 AA; 16031 MW; 563D164AB2802D5 CRC64;

Query Match 15.3%; Score 371.5; DB 4; Length 150;  
 Best Local Similarity 56.6%; Pred. No. 5.9e-22;  
 Matches 73; Conservative 18; Mismatches 37; Indels 1; Gaps 1;  
 QY 1 EVOLQSGPELVKPGASVMISCRISATYFTENTYHWKQSHGESLEWIGINPYGGSIF-60  
 DB 20 QVOLVQSGAEVKKPGASVSKVSGYTLTLPVHWQQAQAGKGLWVGSPDPSPGESIT-79  
 QY 61 SPKFKGKATLTVDRSSSTAYMELSLTSEDSAVYVCARRAGAYEDYWGQSTLTIVSSAK-120  
 DB 80 AREFGQSYTMADTSTDAIMELSLRSDDTAVYCA-VPPDPAFDIMWGQTMVTSAS-138  
 QY 121 TTPPSVYPL-129  
 DB 139 TKGPSVFPL-147

RESULT 12  
 Q95978 PRELIMINARY; PRT; 157 AA.  
 AC Q95978;  
 DT 01-MAY-1999 (Tremblrel, 10, Created)  
 DT 01-MAY-1999 (Tremblrel, 10, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel, 16, Last annotation update)  
 DE VH1 PROTEIN PRECURSOR (FRAGMENT).  
 GN VH1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD;  
 RA Jox A., Zander T., Kuipers R., Irsch J., Kanzler H., Kornacker M.,  
 RA Bohlen H., Diehl V., Wolf J.;  
 RT Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a  
 RT patient with mixed cellularity Hodgkin's disease is associated with  
 RT somatic mutations within the untranslated regions of rearranged and  
 RT class switch recombinant Ig genes";  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AJ005570; CAA06599.1; -.  
 DR InterPro: IPR003006; -.  
 DR InterPro: IPR003596; -.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 KW SIGNAL.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT NON\_TER 157 157  
 SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D8B5 CRC64;

Query Match 15.2%; Score 369.5; DB 4; Length 157;  
 Best Local Similarity 51.9%; Pred. No. 8.9e-22;  
 Matches 70; Conservative 25; Mismatches 35; Indels 5; Gaps 2;  
 QY 1 EVOLQSGPELVKPGASVMISCRISATYFTENTYHWKQSHGESLEWIGINPYGGSIF-60





